

GGGGCCACCG	GGGGTCCCCC	GGGGCGGGGT	AGGGGCGGCC	CCTCACTGCA	CAATGCCAG	60
AGCAGGGGGC	GGAGCCCCAG	CCCCACCCAG	TGCGGAGCGC	GCCGGAGCC	CCGGCCCAAG	120
CTGAGGGCCT	CCGCCCCCCA	GGCGCGCCGG	CGGGGGGCCA	TGTACTCGGG	GAACGGCAGC	180
GGCGGCCACG	GCTACTGGG	GGGGGGGGGG	GGGGGGGGCG	CTGAGGGGCC	GGCGGGGGCG	240
GGGACACTGA	GCCCCCGGCC	CCTCTTCAGC	CCCGGCACCT	ACGAGGGCCT	GGCGCTGCTG	300
CTGGGCTCCA	TTGGGCTGCT	GGGCGTCGG	AACAACCTGC	TGGTGCCTGT	CCTCTACTAC	360
AAGTTCCAGC	GGCTCCGCAC	TCCCACTCAC	CTCCTCCTGG	TCAACATCAG	CCTCAGCGAC	420
CTGCTGGTGT	CCCTCTCGG	GGTCACCTTT	ACCTTCGTGT	CCTGCCTGAG	GAACGGCTGG	480
GTGTGGGACA	CCGTGGGCTG	CGTGTGGGAC	GGGTTTAGCG	GCAGGCTCTT	CGGGATTGTT	540
TCCATTGCCA	CCCTAACCGT	GCTGGCCTAT	GAACGTTACA	TTGGGCTGGT	CCATGCCAGA	600
GTGATCAATT	TTTCCTGGGC	CTGGAGGGCC	ATTACCTACA	TCTGGCTCTA	CTCACTGGCG	660
TGGGCAGGAG	CACCTCTCCT	GGGATGGAAC	AGGTACATCC	TGGACGTTACA	CGGACTAGGC	720
TGCACTGTGG	ACTGGAAATC	CAAGGATGCC	AACGATTCCT	CCTTGTGCT	TTTCTTATTT	780
CTTGGCTGCC	TGGTGGTCCC	CCTGGGTGTC	ATAGCCCATT	GCTATGGCCA	TATTCTATAT	840
TCCATTGAA	TGCTTCGTTG	TGTGGAAGAT	CTTCAGACAA	TTCAAGTGAT	CAAGATTTA	900
AAATATGAAA	AGAAACTGGC	CAAAATGTGC	TTTTAATGA	TATTCACCTT	CCTGGTCTGT	960
TGGATGCCTT	ATATCGTGT	CTGCTTCTTG	TGGTTAATG	GTCATGGTCA	CCTGGTCACT	1020
CCAACAATAT	CTATTGTTTC	GTACCTCTT	GCTAAATCGA	ACACTGTATA	CAATCCAGTG	1080
ATTTATGTCT	TCATGATCAG	AAAGTTCGA	AGATCCCTT	TGCAGCTTCT	GTGCCTCCGA	1140
CTGCTGAGGT	GCCAGAGGCC	TGCTAAAGAC	CTACCAGCAG	CTGGAAGTGA	AATGCAGATC	1200
AGACCCATTG	TGATGTCACA	AAAAGATGGG	GACAGGCCAA	AGAAAAAAAGT	GACTTTAAC	1260
TCTTCTTCCA	TCATTTTAT	CATCACCACT	GATGAATCAC	TGTCAGTTGA	CGACACCCGAC	1320
AAAACCAATG	GGTCAAAGT	TGATGTAATC	CAAGTTCGTC	TTTGTTAGGA	ATGAAGAATG	1380
GCAACGAAAG	ATGGGGCCTT	AAATTGGATG	CCACTTTGG	ACTTTCATCA	TAAGAAGTGT	1440
CTGGAATACC	CGTTCTATGT	AAATCAACA	GAACCTTGTG	GTCCAGCAGG	AAATCCGAAT	1500
TGCCCATATG	CTCTGGGCC	TCAGGAAGAG	GTTGAAC	(SEQ ID NO:1)		1537

FIG.1

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1 MYSGNRSGGH GYWGDGGAAG AEGPAPAGTL SPAPLFSPGT YERLALLGS
51 IGLLGVGNNL LVLVLYYKFQ RLRTPTHLL VNIISLDLLV SLFGVTFTEV
101 SCLRNGWWWD TVGCWWDGFS GSLFGIVSIA TLTIVLAYERY IRVWHARVIN
151 FSWAWRAITY IWLYSLAWAG APLLGWNRYI LDVHGLGCTV DWKSKDANDS
201 SFVLFLFLGC LVVPLGVIAH CYGHILYSIR MLRCVEDLQT IQVIKILKYE
251 KKLAKMCFLM IFTFLVCWMP YIVICFLVN GHCHLVPTI SIVSYLFAKS
301 NTVYNPVIYV FMIRKFRRLSL QLLLCLRLLR CQRPAKDLPA AGSEMQRPI
351 VMSQKDCDRP KKVKTFNSSS IIFIITSDES LSVDDSDKTN GSKVDVIQVR
401 PL (SEQ ID NO:2)

FIG.2

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GGGGCCACGG	GGGGTGCGCC	GGCGCGGGGT	AGCGCGGGCC	CCTCAGTCCA	CAATGCCAG	60
AGCAGGGGGC	GGAGCCCCAG	CCCCACCCAG	TGCGGAGGCC	GCCGCCAGCC	CCGCCCGAAG	120
CTGAGCCCT	CCGCCCCCA	GGCGCGCCGG	GGCCGGGGCC	ATG TAC TCG	GGG AAC	174
				MET TYR SER	GLY ASN	
				1	5	
CGC AGC GGC	GGC CAC GGC	TAC TGG GAC	GGC GGC	GGG GCC	GGC GCT	222
ARG SER GLY	GLY HIS GLY	TYR TRP ASP	GLY GLY GLY	ALA ALA GLY	ALA GLY	
10	15	20				
GAG GGG CCG	GGC CCG GCG	GCG GGG ACA	CTG AGC CCC	GCG CCC CTC	TTC AGC	270
GLU GLY PRO	ALA PRO ALA	GLY THR LEU SER	PRO ALA PRO	LEU PHE SER		
25	30	35				
CCC GGC ACC	TAC GAG CGC	CTG GCG CTG	CTG CTG GGC	TCC ATT GGG	CTG	318
PRO GLY THR	TYR GLU ARG	LEU ALA LEU	LEU GLY SER	ILE GLY LEU		
40	45	50				
CTG GGC GTC	GGC AAC AAC	CTG CTG GTG	CTC CTC TAC	TAC AAG TTC		366
LEU GLY VAL	GLY ASN ASN	LEU LEU VAL	LEU VAL LEU	TYR TYR LYS	PHE	
55	60	65				
CAG CGG CTC	CGC ACT CCC	ACT CAC CTC	CTC CTG GTC	AAC ATC AGC	CTC	414
GLN ARG LEU	ARG THR PRO	THR HIS LEU	LEU LEU VAL	ASN ILE SER	LEU	
70	75	80	85			
AGC GAC CTG	CTG GTG TCC	CTC TTC GGG	GTC ACC TTT	ACC TTC GTG	TCC	462
SER ASP LEU	LEU VAL SER	LEU PHE GLY	VAL THR PHE	THR PHE VAL	SER	
90	95	100				
TGC CTG AGG	AAC GGC TGG	GTC TGG GAC	ACC GTG GGC	TGC GTG TGG	GAC	510
CYS LEU ARG	ASN GLY TRP	VAL TRP ASP	THR VAL GLY	CYS VAL TRP	ASP	
105	110	115				
GGG TTT AGC	GGC AGC CTC	TTC GGG ATT	GTT TCC ATT	GCC ACC CTA	ACC	558
GLY PHE SER	GLY SER LEU	PHE GLY ILE	VAL SER ILE	ALA THR LEU	THR	
120	125	130				
GTC CTG GCC	TAT GAA CGT	TAC ATT CGC	GTC CAT GCC	AGA GTG ATC		606
VAL LEU ALA	TYR GLU ARG	TYR ILE ARG	VAL VAL HIS	ALA ARG VAL	ILE	
135	140	145				

FIG. 3A

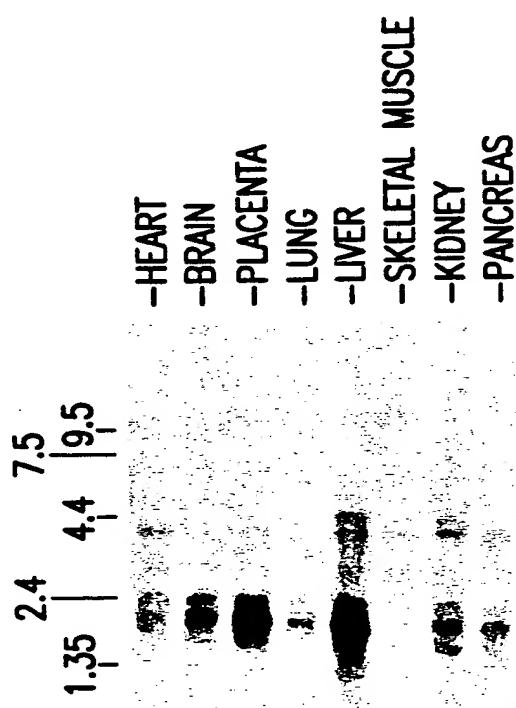
AAT TTT TCC TGG GCC TGG AGG GCC ATT ACC TAC ATC TGG CTC TAC TCA ASN PHE SER TRP ALA TRP ARG ALA ILE THR TYR ILE TRP LEU TYR SER	150 155 160 165	654
CTG GCG TCG GCA GGA GCA CCT CTC CTG GGA TGG AAC AGG TAC ATC CTG LEU ALA TRP ALA GLY ALA PRO LEU LEU GLY TRP ASN ARG TYR ILE LEU	170 175 180	702
GAC GTA CAC GGA CTA GGC TGC ACT GTG GAC TGG AAA TCC AAG GAT GCC ASP VAL HIS GLY LEU GLY CYS THR VAL ASP TRP LYS SER LYS ASP ALA	185 190 195	750
AAC GAT TCC TCC TTT GTG CTT TTC TTA TTT CTT GCC TGC CTG GTG GTG ASN ASP SER SER PHE VAL LEU PHE LEU PHE LEU GLY CYS LEU VAL VAL	200 205 210	798
CCC CTG GGT GTC ATA GCC CAT TGC TAT GGC CAT ATT CTA TAT TCC ATT PRO LEU GLY VAL ILE ALA HIS CYS TYR GLY HIS ILE LEU TYR SER ILE	215 220 225	846
CGA ATG CTT CGT TGT GTG GAA GAT CTT CAG ACA ATT CAA GTG ATC AAG ARG MET LEU ARG CYS VAL GLU ASP LEU GLN THR ILE GLN VAL ILE LYS	230 235 240 245	894
ATT TTA AAA TAT GAA AAC AAA CTG GCC AAA ATG TGC TTT TTA ATG ATA ILE LEU LYS TYR GLU LYS LYS LEU ALA LYS MET CYS PHE LEU MET ILE	250 255 260	942
TTC ACC TTC CTG GTC TGT TGG ATG CCT TAT ATC GTG ATC TGC TTC TTG PHE THR PHE LEU VAL CYS TRP MET PRO TYR ILE VAL ILE CYS PHE LEU	265 270 275	990
GTG GTT AAT GGT CAT GGT CAC CTG GTC ACT CCA ACA ATA TCT ATT GTT VAL VAL ASN GLY HIS GLY HIS LEU VAL THR PRO THR ILE SER ILE VAL	280 285 290	1038
TCG TAC CTC TTT GCT AAA TCG AAC ACT GTA TAC AAT CCA GTG ATT TAT SER TYR LEU PHE ALA LYS SER ASN THR VAL TYR ASN PRO VAL ILE TYR	295 300 305	1086
GTC TTC ATG ATC AGA AAG TTT CGA AGA TCC CTT TTG CAG CTT CTG TGC VAL PHE MET ILE ARG LYS PHE ARG ARG SER LEU LEU GLN LEU LEU CYS	310 315 320 325	1134

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CTC CGA CTG CTG AGG TGC CAG AGG CCT GCT AAA GAC CTA CCA GCA GCT		1182
LEU ARG LEU LEU ARG CYS GLN ARG PRO ALA LYS ASP LEU PRO ALA ALA		
330	335	340
GGA AGT GAA ATG CAG ATC AGA CCC ATT GTG ATG TCA CAG AAA GAT GGG		1230
GLY SER GLU MET GLN ILE ARG PRO ILE VAL MET SER GLN LYS ASP GLY		
345	350	355
GAC AGG CCA AAG AAA AAA GTG ACT TTC AAC TCT TCT TCC ATC ATT TTT		1278
ASP ARG PRO LYS LYS LYS VAL THR PHE ASN SER SER SER ILE ILE PHE		
360	365	370
ATC ATC ACC AGT GAA TCA CTG TCA GTT GAC GAC AGC GAC AAA ACC		1326
ILE ILE THR SER ASP GLU SER LEU SER VAL ASP ASP SER ASP LYS THR		
375	380	385
AAT GGG TCC AAA GTT GAT GTA ATC CAA GTT CGT CCT TTG TAGGAATGAA		1375
ASN GLY SER LYS VAL ASP VAL ILE GLN VAL ARG PRO LEU (SEQ ID NO:2)		
390	395	400
GAATGGCAAC GAAAGATGGG GCCTTAAATT GGATGCCACT TTTGGACTTT CATCATAAGA		1435
AGTGTCTGGA ATACCCGTTTC TATGTAATAT CAACACAACC TTGTGGTCCA GCAGGAAATC		1495
CGAATTGCCCG ATATGCTCTT GGGCCTCAGG AAGACGTTGA AC (SEQ ID NO:2)		1537

FIG. 3C

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2.4 7.5
1.35 4.4 | 9.5

- HEART
- BRAIN
- PLACENTA
- LUNG
- LIVER
- SKELETAL MUSCLE
- KIDNEY
- PANCREAS

FIG. 4A

2.4 7.5
1.35 4.4 | 9.5

- SPLEEN
- THYMUS
- PROSTATE
- TESTIS
- OVARY
- SMALL INTESTINE
- COLON(MUCOSAL LINING)
- PERIPHERAL BLOOD LEUCOCYTE

FIG. 4B

2.4 7.5
1.35 4.4 | 9.5

- AMYGDALA
- COUDATE NUCLEUS
- CORPUS COLLOSUM
- HIPPOCAMPUS
- WHOLE BRAIN
- SUBSTANTIA NIGRA
- THALAMUS

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FIG. 4C**FIG. 4D**

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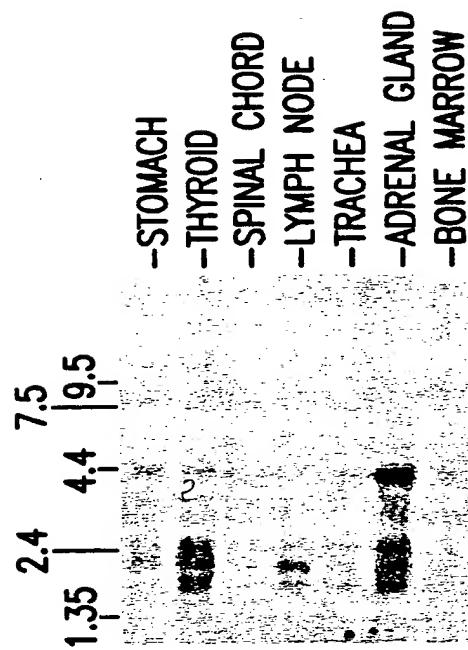


FIG. 4E

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	10	20	30	40	50	60
RHODOPSIN	MNGTECPNFYVPFSNATGVRSPFEYPQQYLAEPWQFSMLAAYMFLIVLGFPINFLTY					

	10	20	30	40	50	60
HC51	NRSGCHGYWDGGAAACAECPAPAGTLSPAPLFSPGTYERLALLGSIGLLGVGNLLVLV					

	70	80	90	100	110	120
RHODOPSIN	VTVQHKKLRTPLNYILLNLAVADLFMVLCGFTSTLYTSLHGYFVFGPTGCNILEGFFATLG					

	70	80	90	100	110	120
HC51	LYYKFQLRRTPTHLLLVNISLSDLLVSLFGVTFVSVCLRNGWWDTVGCVWDGFSGSLF					

	130	140	150	160	170	179
RHODOPSIN	GEIALWSLVVLATERYV-WVCKPMSNFRGENHAIMGVAFTWMALACAAPPLAGWSRYI					

	130	140	150	160	170	180
HC51	GIVSIATLTVLAYERYIRWHRVINFSW---AWRAITYIWLYSLAWAGAPLLGWNRYI					

	180	190	200	210	220	230
RHODOPSIN	PEGLOQSCGIDYYTLKPEVNNESFVIYMFVHFTIPMIIFFCYGQLVFTVKEAAA---					

	190	200	210	220	230
HC51	LDVHGLGCTVDWKS--KDANDSSFLFLGCLVWPLGVIACYGHILYSIRMLRCVEDL				

	240	250	260	270	280	290
RHODOPSIN	QQQESATTQKAKEVTRMVIMVIAFLICWPYASVAFYIFTHQGSNFGP1FMT1PAFFA					

	240	250	260	270	280	290
HC51	QTIQVKILKYEKLAKMCFLMIFTFLVWMPYIVICFLVVNGHHLVTPTISIVSYLFA					

	300	310	320	330	340	
RHODOPSIN	KSAAIYNPVIYIMMKQFRNCMLTTICCGKNPLGDEASATVSKTETSQVAPA (SEQ ID NO:15)					

	300	310	320	330	340	350	(CONTAINED WITHIN SEQ. ID NO:2)
HC51	KSNTVYNPVIYVFMIRKFRSLLQLLCLRLLRCORPAKDLPAAGSEMQIRPVMSQKGDG						

FIG. 5